

SEQUENCE LISTING

<110> Li, Yi
Ruben, Steven, M.

<120> Human G-Protein Chemokine Receptor (CCR5) HDGNR10

<130> 1488.115000P

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<150> 10/127,764

<151> 2002-04-23

<150> 09/502,783

<151> 2000-02-11

<150> 09/339,912

<151> 1999-06-25

<150> 09/195,662

<151> 1998-11-18

<150> 08/466,343

<151> 1995-06-06

<160> 9

<170> PatentIn version 3.0

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ttaattcaat gtagacatct atgtaggcaa ttaaaaacct attgatgtat aaaacagttt 180
gcattcatgg agggcaacta aatacattct aggactttat aaaagatcac tttttattta 240
tgcacagggt ggaacaag atg gat tat caa gtg tca agt cca atc tat gac 291

	Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	
	1				5					10		
atc aat tat tat aca tcg gag ccc tgc caa aaa atc aat gtg aag caa 339	Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln	15	20	25								
atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc atc ttt 387	Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe	30	35	40								
ggc ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac tgc aaa 435	Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys	45	50	55								
agg ctg aag agc atg act gac atc tac ctg ctc aac ctg gcc atc tct 483	Arg Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser	60	65	70								
gac ctg ttt ttc ctt ctt act gtc ccc ttc tgg gct cac tat gct gcc 531	Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala	80	85	90								
gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca ggg ctc 579	Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu	95	100	105								
tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc ctg aca 627	Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr	110	115	120								
atc gat agg tac ctg gct gtc gtc cat gct gtg ttt gct tta aaa gcc 675	Ile Asp Arg Tyr Leu Ala Val Val His Ala Val Phe Ala Leu Lys Ala	125	130	135								
agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg gtg gtg 723	Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val	140	145	150								
gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct caa aaa 771	Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys	160	165	170								
gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt cag tat 819	Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr	175	180	185								
caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg ggg ctg 867	Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu	190	195	200								
gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc cta aaa 915	Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys	205	210	215								
act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct gtg agg 963	Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg	220	225	230								
ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct ccc tac 1011	Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr	240	245	250								

aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc ctg aat 1059
 Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn
 255 260 265

aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg aca gag 1107
 Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu
 270 275 280

act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat gcc ttt 1155
 Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe
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gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa aag cac 1203
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att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa gag gct 1251
 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala
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ccc gag cga gca agc tca gtt tac acc cga tcc act gag gag cag gaa 1299
 Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Glu Glu Gln Glu
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ata tct gtg ggc ttg tgacacggac tcaagtgggc tgggtgaccca gtcagagttg 1354
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Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
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Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
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Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
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Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
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Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
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Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
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Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
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Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
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 35 40 45
 Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu
 50 55 60
 Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu
 65 70 75 80
 Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys
 85 90 95
 Lys Leu Phe Thr Gly Leu Tyr His Ile Arg Tyr Leu Ala Ile Val His
 100 105 110
 Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 115 120 125
 Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 130 135 140
 Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 145 150 155 160
 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 165 170 175
 Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 180 185 190
 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 195 200 205
 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 210 215 220
 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe

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305					310					315					320
Gly	Arg	Gly	Lys	Gly	Lys	Ser	Ile	Gly							
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